

## SEQUENCE LISTING

<110> Goodwin, Avery  
Hoffman, Paul

<120> A Novel Nitroreductase and Therapeutic  
Uses Therefor

<130> DALHO1270WO

<150> 60/080,917

<151> 1998-04-06

<150> 60/081,778

<151> 1998-04-14

<160> 2

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 900

<212> DNA

<213> H. pylori

<400> 1

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aaaaaattct aaaaaaataa aggaaaatca atgaaatttt tggatcagga aaaaagaaga 180
caactattaa acgagcgcca ttcttgcaag atgtttgaca gccattatga gttttctagt 240
gaagaattag aagaaatcgc tgaaatcgcc aggctatcgc caagctctta caacacgcag 300
ccatggcatt ttgtgatggt tactaataag gatttaaaaa aacaaattgc agtgcacagc 360
tactttaatg aagaatgatt aaaagcgctt tcagcggtta tgggtggtagt ctctttaaga 420
cctagcgact tgttaccaca cggccattac atgcaaaacc tttacccgga gtcttataag 480
gttagagtga tcccttcttt tgctcaaagt cttggcctga gattcaacca cagcatgcaa 540
agattagaaa gctatatatt agagcaatgc tatatcgctg tggggcaaat ttgcatgggc 600
gtgagcttaa tgggattgga tagttgcatt attggaggct ttgatccttt aaaagtgggt 660
gaagttttag aagagcgtat caataagcct aaaatcgcat gcttgatcgc tttgggcaag 720
aggggtggcag aagcagagcca aaaatcaaga aaatcaaaag ttgatgcgat tacttggttg 780
tgattaaagca aaatcaaaaa ctttttaact ataatcaaac ctaaattaaa ctttaaggag 840
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<210> 2

<211> 209

<212> PRT

<213> Artificial Sequence

<400> 2

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Met Lys Phe Leu Asp Gln Glu Lys Arg Arg Gln Leu Leu Asn Glu Arg
  1             5             10             15
His Ser Cys Lys Met Phe Asp Ser His Tyr Glu Phe Ser Ser Glu Glu
          20             25             30
Leu Glu Glu Ile Ala Glu Ile Ala Arg Leu Ser Pro Ser Ser Tyr Asn
          35             40             45
Thr Pro Trp His Phe Val Met Val Thr Asn Lys Asp Leu Lys Lys Gln
          50             55             60
Ile Ala Val His Ser Tyr Phe Asn Glu Glu Met Ile Lys Ser Ala Ser
```

WO 99/51270

PCT/US99/07546

2

65					70					75				80
Ala	Leu	Met	Val	Val	Cys	Ser	Leu	Arg	Pro	Ser	Glu	Leu	Leu	Pro His
				85					90					95
Gly	His	Tyr	Met	Gln	Asn	Leu	Tyr	Pro	Glu	Ser	Tyr	Lys	Val	Arg Val
			100					105					110	
Ile	Pro	Ser	Phe	Ala	Gln	Met	Leu	Gly	Val	Arg	Phe	Asn	His	Ser Met
		115					120					125		
Gln	Arg	Leu	Glu	Ser	Tyr	Ile	Leu	Glu	Gln	Cys	Tyr	Ile	Ala	Val Gly
	130					135					140			
Gln	Ile	Cys	Met	Gly	Val	Ser	Leu	Met	Gly	Leu	Asp	Ser	Cys	Ile Ile
145					150				155					160
Gly	Gly	Phe	Asp	Pro	Leu	Lys	Val	Gly	Glu	Val	Leu	Glu	Glu	Arg Ile
			165					170						175
Asn	Lys	Pro	Lys	Ile	Ala	Cys	Leu	Ile	Ala	Leu	Gly	Lys	Arg	Val Ala
		180						185				190		
Glu	Ala	Ser	Gln	Lys	Ser	Arg	Lys	Ser	Lys	Val	Asp	Ala	Ile	Thr Trp
			195				200					205		

Leu

FIGURE 1

1 TGCAGAAATTTTACAGAGAGCCAGATAGCCAAATGCGGGTTTTATTTTAAATTTGAGCAT 60  
61 GGGGCAGATTTTAAAGCTTATTTAGGTAGTTTTCATTTAGGGAATTTTATTTGATGCTAC 120  
121 AAAAAATTTCTAAAAAATAAAGGAAATCAATGAAATTTTGGATCAGGAAAAAAGAAGA 180  
(SD) M K F L D Q E K R R 10  
151 CAACTAATTAAACGAGCGCCATTCTTTGCAAGATGTTTGACAGCCATTATGAGTTTCTTAGT 240  
11 Q L L N E R H S C K M F D S H Y E F S S 30  
241 GAAGAAATTAGAAAGAAATCGCTGAAATCGCCAGGCTATCGCCCAAGCTCTTACAACACGCAG 300  
31 E E L E I A E I A R L S P S S Y N T O 50  
301 CCATGGCAATTTGTGATGGTTACTAATAAGGATTTTAAATAAACAATAATGCGAGTGCACAGC 360  
91 P W H F V M V T N K D L K K Q I A V H S 70  
361 TACTTTAATGAAGAAATGATTAAGAGCGCTTACAGCGTTAATGGTGGTATGCTCTTTAAGA 420  
71 Y F N E E M I K S A S A L M V V C S L R 90  
471 CCTAGCGASTTGTACACACAGCGCCATTACATGCAAAACCTTTACCCGGAGTCTTTATAAG 480  
91 P S E L L P H G H Y M Q N L Y P E S Y K 110  
481 GTTAGAGTGTATCCCTTCTTTTGTCTCAAAATGCTTGGCSTGAGATTCAACCAACA-GCATGCAA 540  
111 V R V I P S F A Q M L G V R F N H S M Q 130  
541 AGATTAGAAAGSTATATTTTAGAGCAATGCTATATCGCTGTGGGCAAAATTTGCATGGGC 600  
131 R L E S Y I L E Q C Y I A V G Q I C M G 150  
601 GTGAGCTTAATGGGATTTGGATAGTTGCAATATTGGAGGSTTTGATCCTTTAAAGTGGGT 660  
151 V S L M G L D S C I I G G F D P L K V G 170  
661 GAAGTTTTAGAAGAGCGGTATCAATAAGCCATAAAATCGCATGCTTGAATCGCTTTGGGCAAG 720  
171 E V L E R I N K P K I A C L I A L G K 190  
721 AGG GTGGCACAAAGCGAGCCAAAAARTCAAGAAATCAAAAAGTTGATGCGATTACTTGGTTG 780  
191 R V A E A S Q K S R K S K V D A I T W L 210  
781 TGATTAAAGCAAAATCAAAAASSTTTTAACTATAATCAAAACCTAAATTAAGTTTAAGGAG 810  
841 TGGCAATTTTGTTTTAAAGAAATGGTTTAAATCGCTCTTTTAGGGGTGTTTTC AAGCGTTTC 900

FIGURE 2

Strain Mtz	1	Deduced Amino Acid Sequence of Rdx	110
26695 S		MKFLQEKRLNRMSCMFDSHYEFSSTELETAELRLSFSINTOPWHFVMTDKDLKQIAHSYFNEEMIKSASALMVVCSLRPSSELLPHGHYMQNLTPESYK	
HP500 S		.....E.....N.....V.....	
HP439 R		.....N.V.N..T.....	
HP1107 R		.....N.V.N..T.....	
HP1134 S		.....E.....F.....N.....K.....S.....	
HP950 S		.....K.....N.....K.....	
HP1043 R		.....H.....H.....AN.....	
Matched Pairs of Mtz <sup>h</sup> /Mtz <sup>s</sup> strains			
10amt3 R		.....E.....N.....	Y.....
10asr1 S		.....E.....N.....	Y.....
12mtz R		.....M.....N.V..V.....T.....	
12asr S		.....M.....N.V..V.....	
Blamt R		.....C.....N.....K.....	
Blasr S		.....N.....N.....K.....	
H2amt R		.....I.S..N.....	
H2csr S		.....I.S..N.....	
21cmt R		.....R..V.N..E.....	S.....
21csr S		.....V.N.....	S.....
111			
26695 S		VRVIPSAQVLGVRFNHSNORLESYTLLECCTIANGQICMGVSLMCLDSCIIGGFDPLKVGVELEERINKPKIACLIALGKRVASQSKRSKVDATWL	210
HP500 S		.....K.....T.Q.....	
HP439 R		.....K.....T.Q.....	
HP1107 R		.....K.....T.Q.....	
HP1134 S		.....T.....I..KLCCD.....	
HP950 S		.....T.....F.IQ.....	
HP1043 R		.....SXCLA.....	
Matched Pairs of Mtz <sup>h</sup> /Mtz <sup>s</sup> strains			
10mt3 R		.....T.....V.....	
10asr1 S		.....T.....	
12mtz R		.....K.....T.....	
12asr S		.....K.....T.....	
Blamt R		.....T.....	
Blasr S		.....S.....K.....C.....	
H2amt R		.....S.....K.....	
H2csr S		.....K.....	
21cmt R		.....K.....	
21csr S		.....K.....	